RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,075

DATE: 10/08/97 TIME: 13:05:11

INPUT SET: S20848.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply Corrected Diskette Needed 1 SEQUENCE LISTING 2 3 General Information: (1) 4 5 (i) APPLICANT: MAERTENS, GEERT 6 STUYVER, LIEVEN 7 (ii) TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES 8 AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC 9 10 **AGENTS** 11 12 (iii) NUMBER OF SEQUENCES: 207 13 14 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: ARNOLD, WHITE & DURKEE 15 (B) STREET: P.O. BOX 4433 16 (C) CITY: HOUSTON 17 (D) STATE: TEXAS 18 (E) COUNTRY: USA 19 20 (F) ZIP: 77210-4433 21 22 (V) COMPUTER READABLE FORM: 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Microsoft Word 6.0 / ASCII text output 26 27 28 (vi) CURRENT APPLICATION DATA: 29 (A) APPLICATION NUMBER: 08/836,075 30 (B) FILING DATE: 21 Apr 1997 31 (vii) PRIOR APPLICATION DATA: 32 (A) APPLICATION NUMBER: PCT/EP95/04155 33 (B) FILING DATE: 23 Oct 1995 34 35 36 (vii) PRIOR APPLICATION DATA: 37 (A) APPLICATION NUMBER: EP 94870166.9 38 (B) FILING DATE: 21 Oct 1994 39 40 (viii) PRIOR APPLICATION DATA: 41 (A) APPLICATION MAMBER: EP 95870076.7 42 (B) FILING DATE: 28 Jun 1995 43 (ix) ATTORNEY/AGENT INFORMATION: 44 45 (A) NAME: KAMMERÈR, PATRICIA A.

RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,075

DATE: 10/08/97 TIME: 13:05:13

INPUT SET: S20848.raw

46 (B) REGISTRATION NUMBER: 29,775

47 (C) REFERENCE/DOCKET NUMBER: INNS:004

48

ERRORED SEQUENCES FOLLOW:

	893	(2) INFORMAT	ION FOR S	EO ID NO	22:	:								
	894													
	895	(1) (i) SEQU	ENCE CHAP	ACTERIST	cics:									
~ >	896) LENGTH:			ids								
>	897 A	W (E) TYPE: a	mino aci	ď									
>	898 ()	(D) TOPOLOG	Y: linea	ìr									
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	900	(ii) MOL	ECULE TYP	E: pepti	.đe									
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>	904	(xi) SEQ	UENCE DES	CRIPTION	i: Sec	OID	NO:	22:						
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	906	Met Ser	Thr Asn	Pro Lys	Pro (31n	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
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	969	Val Gln	Val Lys	Asn Thr	Ser F	His	Ser	Tyr	Met	Vaĺ	Thr	Asn	Asp	Cys

RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,075

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	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175	(xi)	(B (D MOL) TYI) TOI ECULI	PE: 6 POLOG E TYI	GY: [PE:] SCRII	linea pept: PTIO	ar ide N: SI	EQ II	ON C		:						
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176	(xi) Asp 1	(B (D MOL SEQ) TYI) TOI ECULI UENCI	PE: 6 POLOG E TYI E DE: Asn	GY: I PE: 1 SCRII Phe 5	linea pept: PTION	ide N: SI	EQ II) NO: Asn	Leu 10	: Pro	Gly	Cys	Ser	Phe 15	Ser	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177	(xi) Asp 1	(B (D MOL) TYI) TOI ECULI UENCI	PE: 6 POLOG E TYI E DE: Asn	GY: I PE: 1 SCRII Phe 5	linea pept: PTION	ide N: SI	Gly	NO NO Asn	Leu 10	: Pro	Gly	Cys	Ser	Phe 15	Ser	
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	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178	(xi) Asr 1	(B) (D) MOL SEQ Gly) TYI) TOI ECULI UENCI Ile	PE: 6 POLOG E TYI E DE: Asn Leu 20	GY: 3 PE:] SCRII Phe 5	linea pept: PTION Ala Leu	ide N: SI Thr Leu	©Q II Gly Ser	Asn Cys 25	Leu 10 Leu	: Pro Thr	Gly Val	Cys Pro	Ser Ala 30	Phe 15 Ser	Ser Ala	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180	(xi) Asr 1	(B (D MOL SEQ) TYI) TOI ECULI UENCI Ile Leu Tyr	PE: 6 POLOG E TYI E DE: Asn Leu 20	GY: 3 PE:] SCRII Phe 5	linea pept: PTION Ala Leu	ide N: SI Thr Leu	Gly Ser Gly	Asn Cys 25	Leu 10 Leu	: Pro Thr	Gly Val	Cys Pro	Ser Ala 30	Phe 15 Ser	Ser Ala	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181	(xi) Asr 1	(B) (D) MOL SEQ Gly) TYI) TOI ECULI UENCI Ile	PE: 6 POLOG E TYI E DE: Asn Leu 20	GY: 3 PE:] SCRII Phe 5	linea pept: PTION Ala Leu	ide N: SI Thr Leu	©Q II Gly Ser	Asn Cys 25	Leu 10 Leu	: Pro Thr	Gly Val	Cys Pro	Ser Ala 30	Phe 15 Ser	Ser Ala	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181	(xi) Asp 1 Ile	(B) (D) MOL SEQ Gly Phe	TYI TOI UENCI Leu Tyr 35	PE: APOLOGE TY	SCRII Phe 5 Ala Asn	PTION Ala Leu Val	ide N: SI Thr Leu Ser	Gly Ser Gly 40	O NO Asn Cys 25 Ile	Leu 10 Leu Tyr	: Pro Thr	Gly Val	Cys Pro Thr 45	Ser Ala 30 Asn	Phe 15 Ser Asp	Ser Ala Cys	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183	(xi) Asp 1 Ile	(B) (D) MOL SEQ Gly Phe Asn	TYI TOI UENCI Leu Tyr 35	PE: APOLOGE TY	SCRII Phe 5 Ala Asn	PTION Ala Leu Val	ide N: SI Thr Leu Ser	Gly Ser Gly 40	O NO Asn Cys 25 Ile	Leu 10 Leu Tyr	: Pro Thr	Gly Val Val	Cys Pro Thr 45	Ser Ala 30 Asn	Phe 15 Ser Asp	Ser Ala Cys	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1188 1184	(xi) Asp 1 Ile	(B) (D) MOL SEQ Gly Phe	TYI TOI UENCI Leu Tyr 35	PE: APOLOGE TY	SCRII Phe 5 Ala Asn	PTION Ala Leu Val	ide N: SI Thr Leu Ser	Gly Ser Gly 40	O NO Asn Cys 25 Ile	Leu 10 Leu Tyr	: Pro Thr	Gly Val	Cys Pro Thr 45	Ser Ala 30 Asn	Phe 15 Ser Asp	Ser Ala Cys	
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	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186	(xi) Asy 1 Ile Pro	(B) (D) MOL SEQ Gly Phe Asn	TYI) TOI ECULI UENCI Ile Leu Tyr 35 Ser	PE: APOLOGE TYN E TYN E DE: Asn Leu 20 Arg	SCRII Phe 5 Ala Asn Ile	PTION Ala Leu Val Val	ide N: SI Thr Leu Ser Tyr 55	Gly Ser Gly 40 Glu	O NO Asn Cys 25 Ile Ala	Leu 10 Leu Tyr	Pro Thr Tyr His	Gly Val Val His	Cys Pro Thr 45 Ile	Ser Ala 30 Asn Leu	Phe 15 Ser Asp	Ser Ala Cys Leu Trp	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187	(xi) Asr 1 Ile	(B) (D) MOL SEQ Gly Phe Asn Asn 50	TYI) TOI ECULI UENCI Ile Leu Tyr 35 Ser	PE: APOLOGE TYN E TYN E DE: Asn Leu 20 Arg	SCRII Phe 5 Ala Asn Ile	PTION Ala Leu Val	ide N: SI Thr Leu Ser Tyr 55	Gly Ser Gly 40 Glu	O NO Asn Cys 25 Ile Ala	Leu 10 Leu Tyr	: Pro Thr Tyr His	Gly Val Val His	Cys Pro Thr 45 Ile	Ser Ala 30 Asn Leu	Phe 15 Ser Asp	Ser Ala Cys Leu	
	1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186	(xi) Asy 1 Ile Pro Pro 65	(B) (D) MOL SEQ Gly Phe Asn Asn 50	DENCI Leu Tyr 35 Ser	PE: APOLOGE TYPE E TYPE E DE: Asn Leu 20 Arg Ser Val	SCRII Phe 5 Ala Asn Ile	PTION Ala Leu Val Cys 70	ide N: SI Thr Leu Ser Tyr 55	Gly Ser Gly 40 Glu	O NO Asn Cys 25 Ile Ala Glu	Leu 10 Leu Tyr Asp	Pro Thr Tyr His	Gly Val Val His 60	Cys Pro Thr 45 Ile Ser	Ser Ala 30 Asn Leu	Phe 15 Ser Asp His	Ser Ala Cys Leu Trp 80	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/836,075

DATE: 10/08/97 TIME: 13:05:17

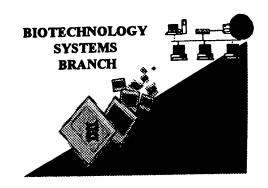
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	1192	Glu Ser Lei	ı Arg Ser His Val	Asp Leu Met Val	. Gly Ala Ala Thr Va	1
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	1194		200	<u>~</u>		
>	1195	Cvs Ser Ala	Teu Tur Ile Clu	Asp Xaa Cys Xa	Gly Leu Phe Leu Val	
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	1197	11.	,	120	123	
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	1203					
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	1206	(i) SPOURN	CE CHARACTERISTICS	. 11110	1	
>	1207	(I) SEQUEN	ENCTH: (447) hage na	ire) 448 N	hour	
/	1207	(R) T	PE: nucleic acid	illb / / · · · /·		
	1209	• •	TRANDEDNESS: singl	Δ		
	1210	, ,	OPOLOGY: linear			
	1211	(2) 1	or oncor: rimear			
	1212	(ii) MOLECU	LE TYPE: cDNA			
	1213	(II) Monneco.	de III'e. CDAA			
	1214	(iii) HYPOTHI	ETTCAL: NO			
	1215	(111) 1111 0111	111011111110			
	1216	(iii) ANTI-SI	ENSE: NO			
	1217	(111) 11111	311021 110			
	1218					
	1219					
	1220	(xi) SEOUENC	CE DESCRIPTION: SE	O ID NO: 31:		
	1221	()				
	1222	GACGGGATCA ATTA	TGCAAC AGGGAACCTT	CCCGGTTGCT CTTT	TTCTAT CTTCCTCTTG	60
	1223					
	1224	GCACTCCTCT CGTG	CCTGAC TGTTCCCGCT	TCGGCCATTA ACTA	CCGCAA CACCTCGGGC	120
	1225					
	1226	ATCTACCACG TCAC	CAATGA CTGCCCGAAC	TCGAGCATAG TTTA	TGAGGC CGACCACCAC	180
	1227					
	1228	ATCTTGCACC TTCC	AGGTTG CGTGCCCTGC	GTGAGAACTG GGAA	TCAGTC ACGTTGCTGG	240
	1229					
	1230	GTGGCCCTTA CTCC	FACCGT CGCAGCGCCA	TACATCGGCG CACC	GCTTGA GTCTCTGCGG	300
	1231					
	1232	AGTCATGTGG ATCT	SATGGT GGGGGCTGCC	ACTGTTTGCT CAGC	CCTTTA CATCGGGGAT	360
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>	1234	TTGTGTGGCG GCTT	CTTCTT GGTTGGTCAG	ATGTTTTCTT TCCG	ACCACCG ACGCCACTGG	(420)42/
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/836,075

DATE: 10/08/97 TIME: 13:05:21

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Line	Error	Original Text
866	Entered (310) and Calc. Seq. Length (0) differ	(A) LENGTH: 310 base pairs
896	Unknown or Misplaced Identifier	(A) LENGTH: 48 amino acids
897	Unknown or Misplaced Identifier	(B) TYPE: amino acid
898	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
904	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
904	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
953	Entered (149) and Calc. Seq. Length (148) differ	(A) LENGTH: 149 amino acids
981	Wrong Amino Acid Designator	Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala er Ala Th
981	Wrong Amino Acid Designator	Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala er Ala Th
1164	Entered (149) and Calc. Seq. Length (148) differ	(A) LENGTH: 149 amino acids
1195	Wrong Amino Acid Designator	Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xa Gly Leu Phe
1207	Entered (447) and Calc. Seq. Length (448) differ	(A) LENGTH: 447 base pairs
1234	# of Sequences for line conflicts w/ running total	TTGTGTGGCG GCTTGTTCTT GGTTGGTCAG ATGTTT



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825). Final rules were published in the Federal Register (55 FR18230) on May 1, 1990, and in the PTO Official Gazette (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

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- Dial-up access through the Internet. Location is ftp://ftp.uspto.gov
 The software is in current directory: pub/checker/
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